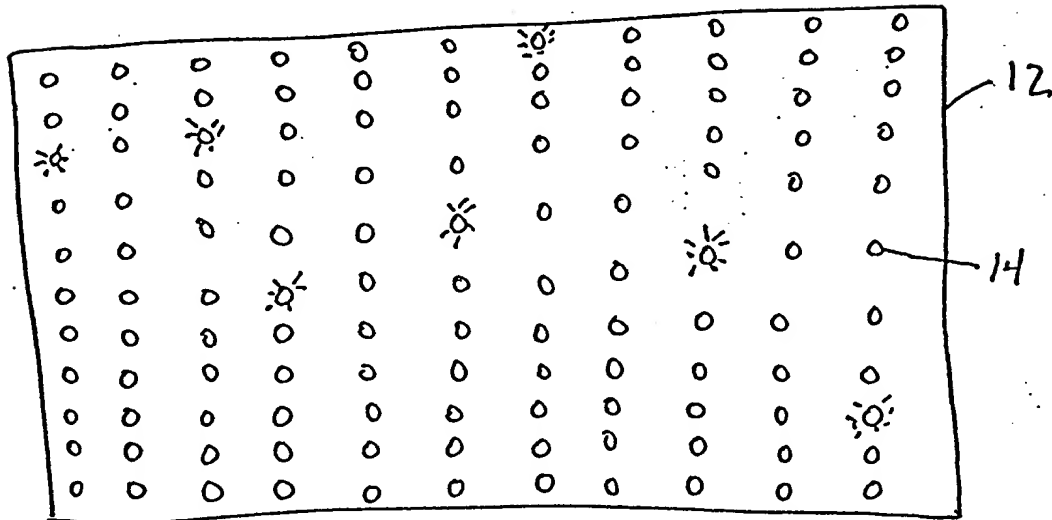
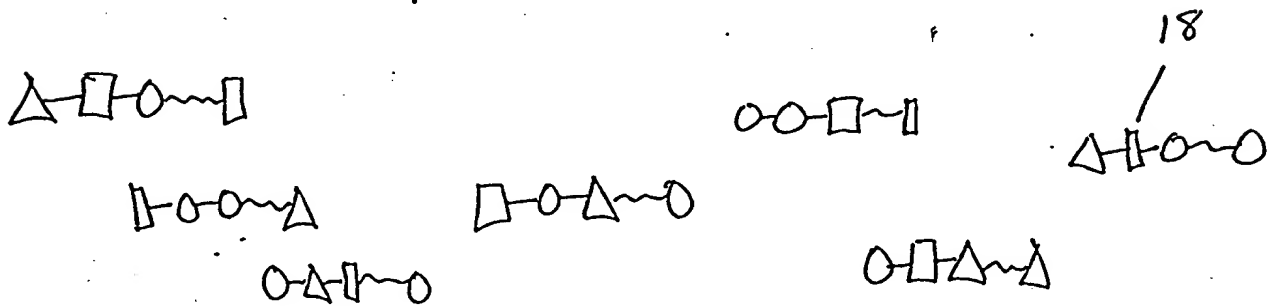


↓ HYBRIDIZATION



↓ SPECTRUM



↓ SEQUENCING

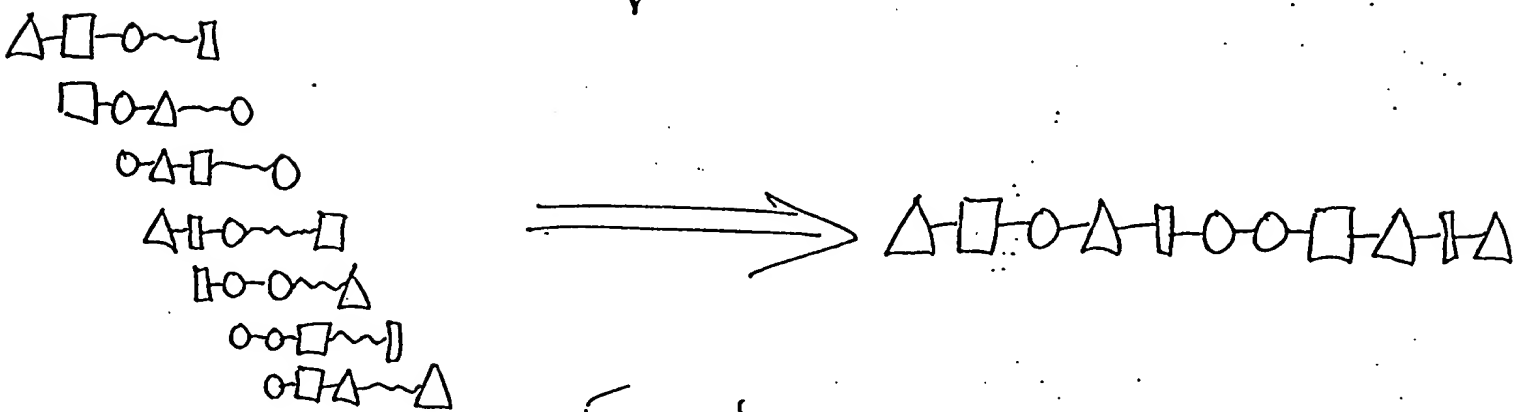


Fig. 1

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Figure 2

Sequence: ACTTACGTTAGCTTATG

(3,1)-Probe Spectrum:

ACT-CACG-A AGC-A

GCT-TGTT-C

CGT-G CTT-G

TAC-TTAG-T TTA-T

(2,2)-Probe Spectrum:

AC-T-A AC-T-C AG-T-A

CG-T-G CT-A-G

GC-T-T GT-A-C

TA-C-T TA-G-T TT-C-T TT-G-T

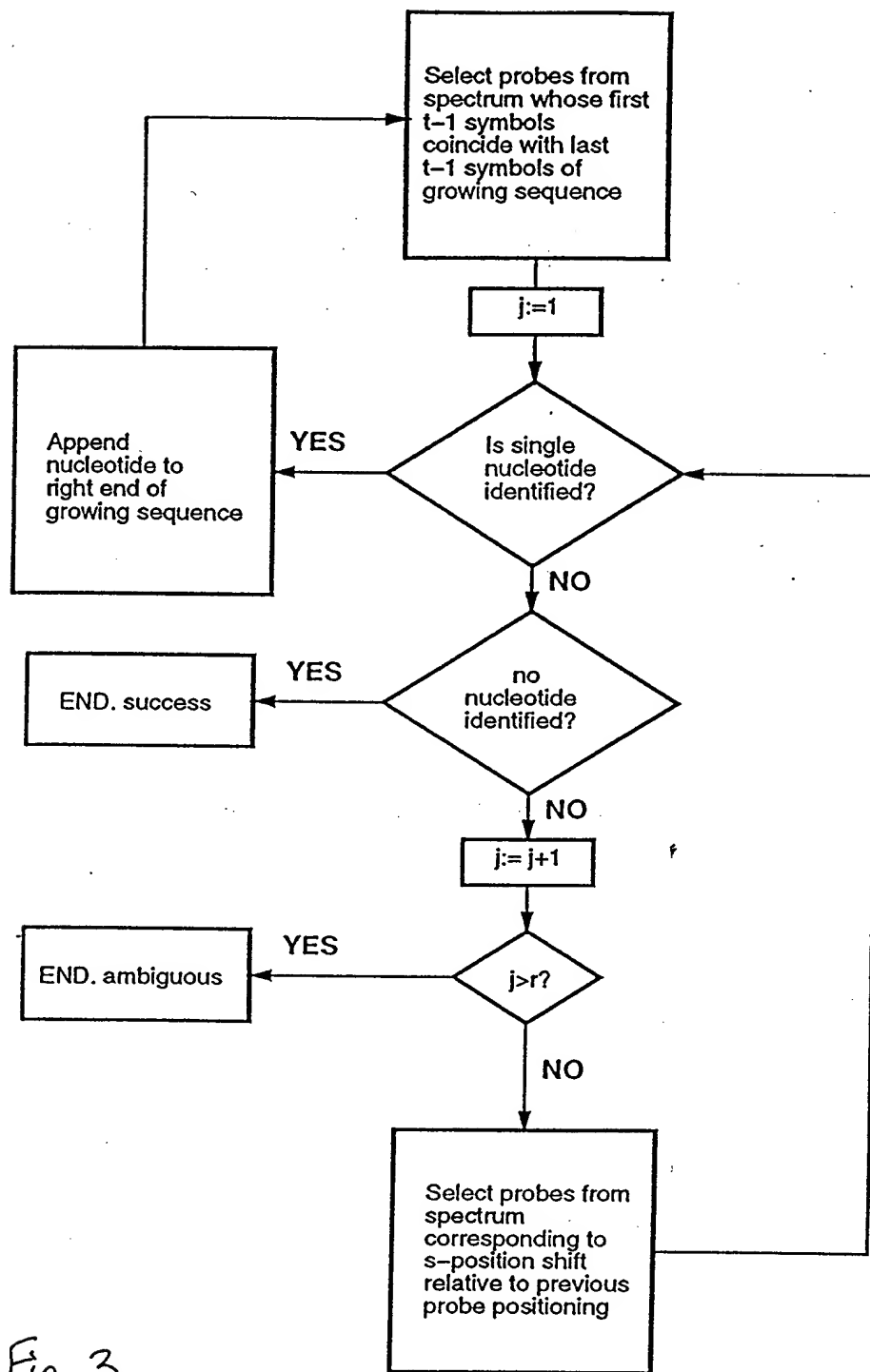


Fig. 3

Figure 4

A.

TAGACCGATA

CGUTUA

ATUGUT

CGUTUG

ATUCUT

B.

TAGACCGATA

CGUTUA

CGUTUG

C.

TAGACCGATA

ATUGUT

ATUCUT

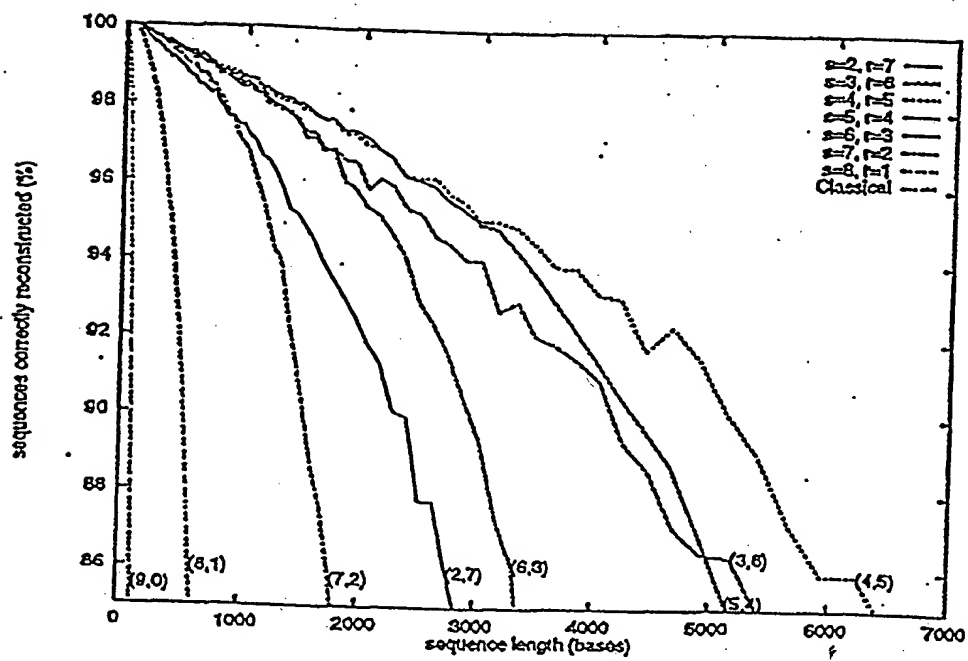


FIG. 5

95 % success rate

(s,r)-pattern	(9,0)	(8,1)	(7,2)	(6,3)	(5,4)	(4,5)	(3,6)	(2,7)
random	101	669	2179	4325	6550	8782	8852	4272
archae	63	305	886	1440	1741	1741	1304	689
e. coli	72	415	1255	2245	3142	3300	2602	1529
haemo	59	321	886	1590	2120	2227	1843	1028

90 % success rate

(s,r)-pattern	(9,0)	(8,1)	(7,2)	(6,3)	(5,4)	(4,5)	(3,6)	(2,7)
random	139	899	2524	5009	7584	10169	10249	4947
archae	86	460	1318	2358	3300	3300	2477	1255
ecoli	97	536	1607	3016	4430	5389	4252	2384
haemo	86	437	1136	2137	2992	3300	3016	1607

FIG. 6

001573 10133
000000 000000

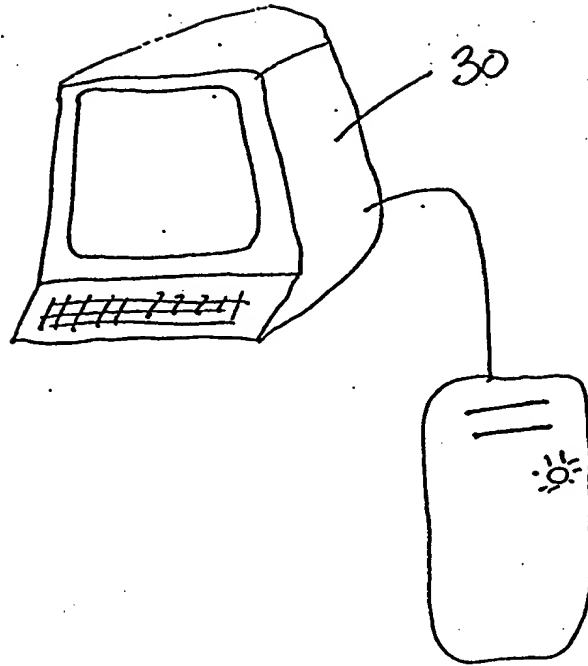
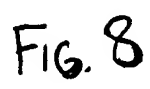


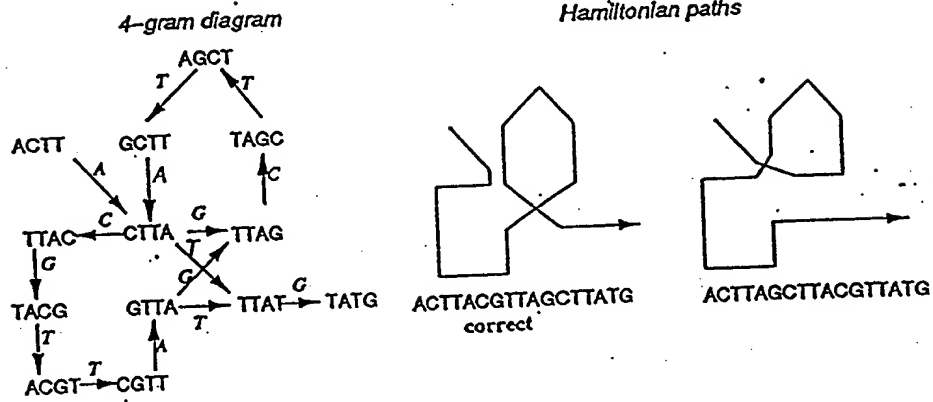
FIG. 7

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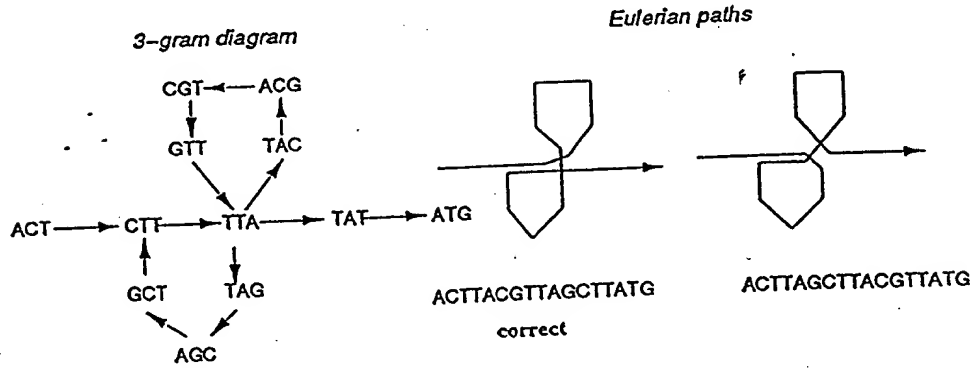


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sequence: ACTTACGTTAGCTTATG



(a)



(b)

Fig. 9

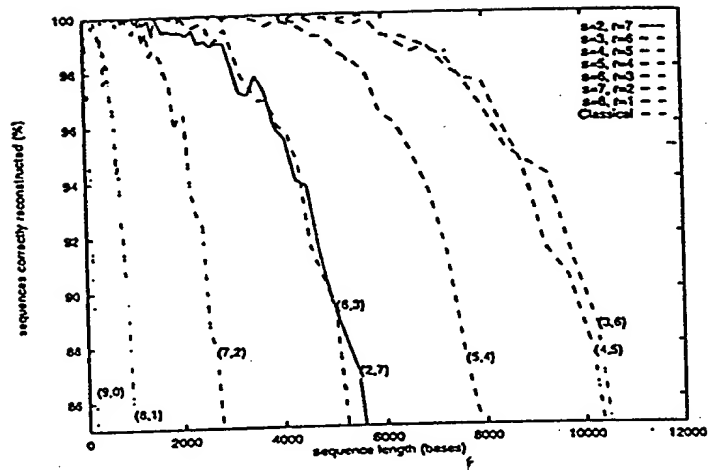


Fig. 10